

IN THE CLAIMS:

*Please amend withdrawn claim 1 and pending claim 13 as shown below.*

1. (Withdrawn - currently amended) A method of detecting *Mycobacterium* species present in a biological sample, comprising the steps of:

providing a biological sample containing nucleic acid from at least one *Mycobacterium* species comprising a *Mycobacterium* 16S ribosomal RNA (rRNA) or DNA encoding a *Mycobacterium* 16S rRNA;

amplifying the *Mycobacterium* 16S rRNA or *Mycobacterium* DNA encoding the *Mycobacterium* 16S rRNA in an *in vitro* nucleic acid amplification mixture comprising at least one polymerase activity, and a combination of at least two primers selected from the group consisting of a first primer of SEQ ID NO:11 and a second primer that is one first oligonucleotide and at least one second oligonucleotide, wherein the first oligonucleotide consists of a promoter sequence and a sequence that hybridizes to a *Mycobacterium* 16S rRNA or DNA sequence, and the second oligonucleotide is an oligonucleotide consisting of 19 to 25 bases that contains made up of contiguous bases 1 to 18 of SEQ ID NO:24 and optionally three to seven bases 5' to the contiguous bases 1 to 18 of SEQ ID NO:24 and/or optionally one base 3' to the contiguous bases 1 to 18 of SEQ ID NO:24 to produce amplified *Mycobacterium* nucleic acid; and  
detecting the amplified *Mycobacterium* nucleic acid by detecting a label associated with the amplified *Mycobacterium* nucleic acid.

2. (Withdrawn - Original) The method of Claim 1, further comprising in the steps of:  
adding to the biological sample at least one capture oligonucleotide that

specifically  
hybridizes to the *Mycobacterium* 16S rRNA and an immobilized nucleic acid that  
hybridizes to  
the capture oligonucleotide under hybridizing conditions to produce a hybridization  
complex;  
and  
separating the hybridization complex from other components of the biological  
sample before the amplifying step.

3. (Withdrawn - Original) The method of Claim 1, wherein the amplifying step  
amplifies 16S rRNA or DNA encoding 16S rRNA from *M. tuberculosis* or a  
*Mycobacterium* other than *tuberculosis* (MOTT) species.
4. (Withdrawn - Original) The method of Claim 1, wherein the amplifying step  
amplifies 16S rRNA or DNA encoding 16S rRNA from *M. abscessus*, *M. africanum*, *M.*  
*asiaticum*, *M. avium*, *M. bovis*, *M. celatum*, *M. chelonae*, *M. flavescens*, *M. fortuitum*, *M.*  
*gastr*, *M. gordonae*, *M. haemophilum*, *M. intracellulare*, *M. interjectum*, *M. intermedium*,  
*M. kansasii*, *M. malmoense*, *M. marinum*, *M. non-chromogenicum*, *M. paratuberculosis*,  
*M. phlei*, *M. scrofulaceum*, *M. shimodei*, *M. simiae*, *M. smegmatis*, *M. szulgai*, *M. terrae*,  
*M. triviale*, *M. tuberculosis*, *M. ulcerans* or *M. xenopi*.
5. (Withdrawn - Original) The method of Claim 1, wherein the detecting step uses at  
least one probe that hybridizes specifically to the amplified *Mycobacterium* nucleic acid.
6. (Withdrawn - Original) The method of Claim 5, wherein the detecting step uses at  
least one labeled probe that hybridizes specifically to the amplified *Mycobacterium*  
nucleic acid.

7. (Withdrawn - Original) The method of Claim 5, wherein the detecting step uses a plurality of probes that hybridize specifically to the amplified *Mycobacterium* nucleic acid.

8. (Withdrawn - Previously amended) The method of Claim 1, wherein the amplifying step uses a combination of at least a first primer and a second primer, wherein the first primer consists of SEQ ID NO:11, and the second primer is selected from the group consisting of SEQ ID NO:21, SEQ NO:22, SEQ ID NO:23 and SEQ ID NO:24.

9. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:21.

10. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:22.

11. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:23.

12. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:24.

13. (Currently amended) A composition for amplifying in an in vitro amplification reaction a *Mycobacterium* 16S rRNA sequence or a DNA encoding 16S rRNA, comprising a combination of at least ~~two oligonucleotides~~ one first oligonucleotide and at least one second oligonucleotide, wherein ~~[[a]] the~~ first oligonucleotide ~~contains~~ consists of a promoter sequence and a sequence that hybridizes to a *Mycobacterium* 16S rRNA or DNA sequence, and ~~[[a]] wherein the~~ second oligonucleotide is an

oligonucleotide consisting of 19 to 25 bases ~~that contains~~ made up of contiguous bases 1 to 18 of SEQ ID NO:24 and optionally three to seven bases 5' to the contiguous bases 1 to 18 of SEQ ID NO:24 and/or optionally one base 3' to the contiguous bases 1 to 18 of SEQ ID NO:24.

14. (Previously amended) The composition of Claim 13, wherein the composition comprises:

at least one first oligonucleotide consisting of SEQ ID NO:11, and

at least one second oligonucleotide consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 or SEQ ID NO:24.

15. (Previously amended) The composition of Claim 14, wherein the composition comprises:

the at least one first oligonucleotide consisting of SEQ ID NO:11, and

the at least one second oligonucleotide consisting of SEQ ID NO:21.

16. (Previously amended) A kit containing one or more oligonucleotides selected from the group consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24.

17. (Previously amended) The kit of claim 16, further containing an oligonucleotide consisting of SEQ ID NO:11.

18. (Previously amended) The kit of claim 17, containing

a first oligonucleotide consisting of SEQ ID NO:11, and

at least one second oligonucleotide consisting of SEQ ID NO:21, SEQ ID NO:22, or SEQ ID NO:23.

19. (Previously amended) The composition of Claim 14, wherein the composition comprises:

the at least one first oligonucleotide consisting of SEQ ID NO:11, and  
the at least one second oligonucleotide consisting of SEQ ID NO:23.

20. (Previously amended) The composition of Claim 14, wherein the composition comprises:

the at least one first oligonucleotide consisting of SEQ ID NO:11, and  
the at least one second oligonucleotide consisting of SEQ ID NO:24.